1646

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RAW SEQUENCE LISTING   DATE: 02/04/2002
PATENT APPLICATION: US/09/525,998A   TIME: 11:33:32

Input Set : A:\98385Eseq.txt
Output Set: N:\CRF3\02042002\I525998A.raw

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 3  <110> APPLICANT: Hauptmann, Rudolph
 4         Himmler, Adolph
 5         Maurer-Fogy, Ingrid
 6         Stratowa, Christian
 8  <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
 9         Them
11  <130> FILE REFERENCE: 98-385-E
13  <140> CURRENT APPLICATION NUMBER: 09/525,998A
14  <141> CURRENT FILING DATE: 2000-03-15
16  <150> PRIOR APPLICATION NUMBER: 08/383,676
17  <151> PRIOR FILING DATE: 1995-02-01
19  <150> PRIOR APPLICATION NUMBER: 08/153,287
20  <151> PRIOR FILING DATE: 1993-11-17
22  <150> PRIOR APPLICATION NUMBER: 07/821,750
23  <151> PRIOR FILING DATE: 1993-01-02
25  <150> PRIOR APPLICATION NUMBER: 07/511,430
26  <151> PRIOR FILING DATE: 1990-04-20
28  <160> NUMBER OF SEQ ID NOS: 97
30  <170> SOFTWARE: PatentIn Ver. 2.0
32  <210> SEQ ID NO: 1
33  <211> LENGTH: 1368
34  <212> TYPE: DNA
35  <213> ORGANISM: Homo sapiens
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38  <221> NAME/KEY: CDS
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42  <221> NAME/KEY: sig_peptide
43  <222> LOCATION: (1)..(87)
45  <220> FEATURE:
46  <221> NAME/KEY: misc_feature
47  <222> LOCATION: (88)..(120)
48  <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
49         extracellular proteases following secretion
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52  <221> NAME/KEY: misc_feature
53  <222> LOCATION: (606)..(633)
54  <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
55         extracellular proteases following secretion
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60   1               5                   10                  15
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62  gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct   96
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64          20                  25                  30

66  cac cta ggg gac agg gag aag aaa gat agt gtg tgt ccc caa gga aaa   144
67  His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
68          35                  40                  45

70  tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa   192
71  Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
72          50                  55                  60

74  gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac   240
75  Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
76      65                  70                  75                  80

78  tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc   288
79  Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
80                  85                  90                  95

82  aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg   336
83  Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
84          100                 105                 110

86  gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg   384
87  Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
88          115                 120                 125

90  aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc   432
91  Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
92          130                 135                 140

94  aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag   480
95  Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
96  145                 150                 155                 160

98  aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa   528
99  Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
100                 165                 170                 175

102 aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg   576
103 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
104                 180                 185                 190

106 aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca   624
107 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
108         195                 200                 205

110 ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt   672
111 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
112         210                 215                 220

114 tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag   720
115 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
116 225                 230                 235                 240

118 tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag   768
119 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
120                 245                 250                 255

122 ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc   816
123 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
124                 260                 265                 270

126 ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg   864
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127 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
128         275             280             285
130 ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt      912
131 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
132         290             295             300
133 ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg      960
135 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
136 305             310             315                 320
138 gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gat ccc atc ccc aac     1008
139 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
140             325             330             335
142 ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac     1056
143 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
144             340             345             350
146 act gat gac ccc gcg acg ctg tac gcc gtg gtg gaa aac gtg ccc ccg     1104
147 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
148         355             360             365
150 ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag     1152
151 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
152     370             375             380
154 atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa     1200
155 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
156 385             390             395                 400
158 tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc     1248
159 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
160             405             410             415
162 acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc     1296
163 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
164             420             425             430
166 tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg     1344
167 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
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170 ccc gcg ccc agt ctt ctc aga tga                                     1368
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172     450             455
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176 <211> LENGTH: 455
177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
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184 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
185             20              25              30
187 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
188         35              40              45
190 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
191     50              55              60
193 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
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194  65                    70                  75                  80
196  Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
197              85                  90                  95
199  Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
200             100                 105                 110
202  Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
203             115                 120                 125
205  Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
206         130                 135                 140
208  Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
209  145                 150                 155                 160
211  Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
212                 165                 170                 175
214  Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
215             180                 185                 190
217  Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
218             195                 200                 205
220  Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
221         210                 215                 220
223  Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
224  225                 230                 235                 240
226  Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
227                 245                 250                 255
229  Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
230             260                 265                 270
232  Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
233             275                 280                 285
235  Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
236         290                 295                 300
238  Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
239  305                 310                 315                 320
241  Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
242                 325                 330                 335
244  Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
245             340                 345                 350
247  Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
248         355                 360                 365
250  Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
251         370                 375                 380
253  Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
254  385                 390                 395                 400
256  Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
257             405                 410                 415
259  Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
260             420                 425                 430
262  Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
263         435                 440                 445
265  Pro Ala Pro Ser Leu Leu Arg
266  450                 455
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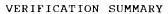
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276 <222> LOCATION: (1)..(483)
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281  1               5                  10                  15
283 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt      96
284 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
285          20                  25                  30
287 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc     144
288 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
289          35                  40                  45
291 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa     192
292 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
293          50                  55                  60
295 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac     240
296 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
297  65                  70                  75                  80
299 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg     288
300 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
301              85                  90                  95
303 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg     336
304 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
305              100                 105                 110
307 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc     384
308 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
309              115                 120                 125
311 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac     432
312 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
313          130                 135                 140
315 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag     480
316 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
317 145                 150                 155                 160
319 aat                                                                 483
320 Asn
323 <210> SEQ ID NO: 4
324 <211> LENGTH: 161
325 <212> TYPE: PRT
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332 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
333          20                  25                  30
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VERIFICATION SUMMARY   DATE: 02/04/2002
PATENT APPLICATION: US/09/525,998A   TIME: 11:33:33

Input Set : A:\98385Eseq.txt
Output Set: N:\CRF3\02042002\I525998A.raw

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L:1643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
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L:2525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
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